

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/876,478

DATE: 07/19/2001

TIME: 09:28:23

Input Set : A:\Pto.amc

Output Set: N:\CRF3\07192001\I876478.raw

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6 <110> APPLICANT: Peyman, John A.
8 <120> TITLE OF INVENTION: Interferon-Suppressing Placental Lactogen Peptides
10 <130> FILE REFERENCE: 1101
W--> 12 <140> CURRENT APPLICATION NUMBER: US/09/876,478
12 <141> CURRENT FILING DATE: 2001-06-07
14 <150> PRIOR APPLICATION NUMBER: 60/210,082
16 <151> PRIOR FILING DATE: 2000-06-07
18 <160> NUMBER OF SEQ ID NOS: 16
20 <170> SOFTWARE: MS-DOS
24 <210> SEQ ID NO: 1
26 <211> LENGTH: 789
28 <212> TYPE: DNA
30 <213> ORGANISM: HOMO SAPIENS
32 <220> FEATURE:
34 <222> LOCATION:
36 <223> OTHER INFORMATION: hPL(1-28) cDNA
38 <400> SEQUENCE: 1
40 ctgttgacag ctcacctagc ggcaatggct gcaggtccc ggacgtccct 50
42 gctcctggct tttgccctgc tctgctgccc ctggcttcaa gaggtgggtg 100
44 cgttcctaac cgttcctgta tccaggtttt ttgaccacgc tatgtcccaa 150
46 gccatcgcg cgcaccagct ggccattgac acctactagg agtttgaaga 200
48 aacctatata ccaaaggacc agaagtattc attcctgcat gactcccaaga 250
50 cctccttctg cttctcagac tctattccga caccctccaa catggaggaa 300
52 acgcaacaga aatccaatct agagctgctc cgcattctcc tgcgtctcat 350
54 cqaatcgttg ctggagcccg tgcggttctt caggaatatg ttgcgcaaca 400
56 acctggtgta tgacacctcg gacagcgatg actatcacct cctaaaggac 450
58 ctgaggaag gcatccaaac gctgatgggg aggctggaag acggcagccg 500
60 cgggactggg cagatcctca agcagacctc cagcaagttt gacacaaact 550
62 cgcacaacca tgacgcactg ctcaagaact acgggctgct ctactgttct 600
64 aggaaggaca tggacaaggt cgagacattc ctgcgcattg tgcagtgcgc 650
66 ctctgtggag ggcagctgtg gcttctaggt gcccgctggg catcctgtga 700
68 ccgacccttc cccagtgcct ctctggccc ctggaagggt ccactcagtg 750
70 cccatcagcc ttgtcctaataaaaattagttgtatcatc 789
74 <210> SEQ ID NO: 2
76 <211> LENGTH: 54
78 <212> TYPE: PRT
80 <213> ORGANISM: HOMO SAPIENS
82 <220> FEATURE:
84 <223> OTHER INFORMATION: hPL(1-28) signal sequence and secreted peptide, or N-terminal
54 residues
85 of hPL-3
87 <400> SEQUENCE: 2
89 Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Ala Leu
90 5 10 15
92 Leu Cys Leu Pro Trp Leu Gln Glu Ala Gly Ala Val Gln Thr Val
93 20 25 30
95 Pro Leu Ser Arg Leu Phe Asp His Ala Met Leu Gln Ala His Arg
96 35 40 45

```

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98 Ala His Gln Leu Ala Ile Asp Thr Tyr

99 50

103 &lt;210&gt; SEQ ID NO: 3

105 &lt;211&gt; LENGTH: 54

107 &lt;212&gt; TYPE: PRT

109 &lt;213&gt; ORGANISM: HOMO SAPIENS

111 &lt;220&gt; FEATURE:

113 &lt;223&gt; OTHER INFORMATION: N-terminal 54 residues of hPL-4

115 &lt;400&gt; SEQUENCE: 3

117 Met Ala Pro Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Ala Leu

118 5 10 15

120 Leu Cys Leu Pro Trp Leu Gln Glu Ala Gly Ala Val Gln Thr Val

121 20 25 30

123 Pro Leu Ser Arg Leu Phe Asp His Ala Met Leu Gln Ala His Arg

124 35 40 45

127 Ala His Gln Leu Ala Ile Asp Thr Tyr

128 50

132 &lt;210&gt; SEQ ID NO: 4

134 &lt;211&gt; LENGTH: 28

136 &lt;212&gt; TYPE: PRT

138 &lt;213&gt; ORGANISM: HOMO SAPIENS

140 &lt;220&gt; FEATURE:

142 &lt;223&gt; OTHER INFORMATION: hPL(1-28) peptide

144 &lt;400&gt; SEQUENCE: 4

146 Val Gln Thr Val Leu Ser Arg Leu Phe Lys Glu Ala Met Leu

147 5 10 15

149 Gln Ala His Arg Ala His Gln Leu Ala Ile Asp Thr Tyr

150 20 25

154 &lt;210&gt; SEQ ID NO: 5

156 &lt;211&gt; LENGTH: 162

158 &lt;212&gt; TYPE: DNA

160 &lt;213&gt; ORGANISM: HOMO SAPIENS

162 &lt;220&gt; FEATURE:

164 &lt;223&gt; OTHER INFORMATION: cDNA construct coding for signal sequence and secreted peptide of hPL(1-

165 28)

167 &lt;400&gt; SEQUENCE: 5

169 atggctccag gctcccggac gtccctgctc ctggcttttg cctgctctg 50

171 cctgccctgg ctccaagagg ctggtgccgt ccaaaccgtt ccgttatcca 100

173 qgcctttttga ccacgctatg ctccaagccc atcgcgcgca ccagctggcc 150

175 attgacacct ac 162

179 &lt;210&gt; SEQ ID NO: 6

181 &lt;211&gt; LENGTH: 54

183 &lt;212&gt; TYPE: PRT

185 &lt;213&gt; ORGANISM: HOMO SAPIENS

187 &lt;220&gt; FEATURE:

189 &lt;223&gt; OTHER INFORMATION: N-terminal 54 residues of hPL-4

191 &lt;400&gt; SEQUENCE: 6

193 Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Ala Leu

194 5 10 15

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196 Leu Cys Leu Pro Trp Leu Gln Glu Ala Gly Ala Val Gln Thr Val
197                20                25                30
199 Pro Leu Ser Arg Leu Phe Lys Glu Ala Met Leu Gln Ala His Arg
200                35                40                45
202 Ala His Gln Leu Ala Ile Asp Thr Tyr
203                50
207 <210> SEQ ID NO: 7
209 <211> LENGTH: 28
211 <212> TYPE: PRT
213 <213> ORGANISM: HOMO SAPIENS
215 <220> FEATURE:
217 <223> OTHER INFORMATION: hPL-1(1-28) peptide
219 <400> SEQUENCE: 7
221 Val Gln Thr Val Pro Leu Ser Arg Leu Phe Lys Glu Ala Met Leu
222                5                10                15
224 Gln Ala His Arg Ala His Gln Leu Ala Ile Asp Thr Tyr
225                20                25
229 <210> SEQ ID NO: 8
231 <211> LENGTH: 162
233 <212> TYPE: DNA
235 <213> ORGANISM: HOMO SAPIENS
237 <220> FEATURE:
239 <223> OTHER INFORMATION: cDNA construct coding for signal sequence and secreted
peptide of hPL-1(1-
240                28)
242 <400> SEQUENCE: 8
244 atggctgcag gctcccgag gtcctgctc ctggcttttg cctgctctg      50
246 cctgccctgg cttcaagagg ctggtgccgt ccaaaccgtt cccttatcca    100
248 ggctttttta agaggctatg tccaagccc atcgcgacaca ccagctggcc    150
250 attgacacct ac                                     162
254 <210> SEQ ID NO: 9
256 <211> LENGTH: 87
258 <212> TYPE: DNA
260 <213> ORGANISM: HOMO SAPIENS
262 <220> FEATURE:
264 <223> OTHER INFORMATION: hPL(1-28) 87-mer oligo
266 <400> SEQUENCE: 9
268 atggctccag gctcccgag gtcctgctc ctggcttttg cctgctctg      50
270 cctgccctgg cttcaagagg ctggtgccgt ccaaacc                                     87
274 <210> SEQ ID NO: 10
276 <211> LENGTH: 85
278 <212> TYPE: DNA
280 <213> ORGANISM: HOMO SAPIENS
282 <220> FEATURE:
284 <223> OTHER INFORMATION: hPL(1-28) 85-mer oligo
286 <400> SEQUENCE: 10
288 gtaggtgtca atggccagct ggtgcgcgcg atgggcttgg agcatagcgt      50
290 ggtcaaaaag cctggataac ggaacggttt ggacg                                     85
294 <210> SEQ ID NO: 11
296 <211> LENGTH: 85

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298 <212> TYPE: DNA
300 <213> ORGANISM: HOMO SAPIENS
302 <220> FEATURE:
304 <223> OTHER INFORMATION: hPL-1(1-28) 85-mer oligo
306 <400> SEQUENCE: 11
308 gtagatgta atggccagct ggtgtgcgcg atgggcttgg agcatagcct 50
310 ctlttaaaaag cctggataag ggaacgggtt ggacg 85
314 <210> SEQ ID NO: 12
316 <211> LENGTH: 24
318 <212> TYPE: DNA
320 <213> ORGANISM: ARTIFICIAL SEQUENCE
322 <220> FEATURE:
324 <223> OTHER INFORMATION: pSH4-1
326 <400> SEQUENCE: 12
328 gatgttgccct tactttctag gcct 24
332 <210> SEQ ID NO: 13
334 <211> LENGTH: 24
336 <212> TYPE: DNA
338 <213> ORGANISM: ARTIFICIAL SEQUENCE
340 <220> FEATURE:
342 <223> OTHER INFORMATION: pSH4-2
344 <400> SEQUENCE: 13
346 aactcatcaa tgtatcttat catg 24
350 <210> SEQ ID NO: 14
352 <211> LENGTH: 54
354 <212> TYPE: PRT
356 <213> ORGANISM: HOMO SAPIENS
358 <220> FEATURE:
360 <223> OTHER INFORMATION: N-TERMINAL 54 RESIDUES OF HGH-1
362 <400> SEQUENCE: 14
364 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu
365 5 10 15
367 Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile
368 20 25 30
370 Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg
371 35 40 45
373 Leu His Gln Leu Ala Phe Asp Thr Tyr
374 50
378 <210> SEQ ID NO: 15
380 <211> LENGTH: 56
382 <212> TYPE: PRT
384 <213> ORGANISM: HOMO SAPIENS
386 <220> FEATURE:
388 <223> OTHER INFORMATION: N-TERMINAL 56 RESIDUES OF HGH-V
390 <400> SEQUENCE: 15
392 Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu
393 5 10 15
395 Leu Cys Leu Ser Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile
396 20 25 30

```

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398 Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala Arg Asp
399                      35                      40                      45
401 Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr
402                      50                      55
406 <210> SEQ ID NO: 16
408 <211> LENGTH: 56
410 <212> TYPE: PRT
412 <213> ORGANISM: HOMO SAPIENS
414 <220> FEATURE:
416 <223> OTHER INFORMATION: N-TERMINAL 56 RESIDUES OF HPRL
418 <400> SEQUENCE: 16
420 Met Asn Ile Lys Gly Ser Pro Trp Lys Gly Ser Leu Leu Leu Leu
421                      5                      10                      15
423 Leu Val Ser Asn Leu Leu Leu Cys Gln Ser Val Ala Pro Leu Pro
424                      20                      25                      30
426 Ile Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu Arg Asp
427                      35                      40                      45
429 Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr
430                      50                      55

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VERIFICATION SUMMARY

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L:12 M:282 W: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER is Added.